

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 21:05:24 ; Search time 8498.8 Seconds
(Without alignments)
30.345 Million cell updates/sec

Title: US-09-851-670-2

Perfect score: 24
Sequence: 1 cgacaatggaataaacagctgcgc 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 537289281 residues

Total number of hits satisfying chosen parameters: 111874

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_estin:*
3: em_estin:*
4: em_estin:*
5: em_estin:*
6: em_estin:*
7: em_estin:*
8: em_estin:*
9: em_estin:*
10: em_estin:*
11: em_estin:*
12: em_estin:*
13: em_estin:*
14: em_estin:*
15: em_estin:*
16: em_estin:*
17: em_estin:*
18: em_estin:*
19: em_estin:*
20: em_estin:*
21: em_estin:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.6	60.8	40	10	AI619480 ty38g04.x
2	14.4	60.0	50	10	AU104403 AU104403
3	14.4	60.0	55	10	AI357794 qu98e04.x
4	14	58.3	45	13	AZ662129 IM0541J06
5	13.8	57.5	49	13	AZ810540 2M0076E08
6	13.6	56.7	29	13	AZ831178 2M0110I18
7	13.4	55.8	31	10	AI746720 u106f05.y
8	13.4	55.8	46	10	AI026096 ov94h09.s
9	13.4	55.8	53	13	AZ576214 AST-TD13S
10	13.4	55.8	55	11	R60882 yh08f11.r1
11	13.2	55.0	27	13	AZ795938 2M0051K23
12	13.2	55.0	38	11	C21091 HUMGS000260

13	13.2	55.0	59	10	AA66844 vm5g11.s
14	13.2	55.0	60	10	AI966547 701667389
15	13	54.2	34	10	AA476000 vb26a02.r
16	13	54.2	50	10	AU104180 AU104180
17	13	54.2	50	10	AU104183 AU104183
18	13	54.2	50	10	AU104194 AU104194
19	13	54.2	54	11	T50983 yb71c06.s1
20	13	54.2	54	13	AZ783216 2M0024011
21	12.8	53.3	50	11	BC939021 cm30a04.y
22	12.8	53.3	52	10	TA309602P
23	12.8	53.3	53	10	AA528415
24	12.8	53.3	54	5	AW284534 LG1-270.C
25	12.8	53.3	58	11	W41141 mc38h02.r1
26	12.8	53.3	60	10	AV518812 AV518812
27	12.6	52.5	25	10	AI620546 tu95b04.x
28	12.6	52.5	40	10	AI972180 w763e10.x
29	12.6	52.5	44	13	AZ798809 2M00551L6
30	12.6	52.5	52	10	AI000127 os43a10.s
31	12.6	52.5	58	11	BG273140 na134f09.
32	12.4	51.7	38	10	AV836261 AV836261
33	12.4	51.7	46	10	AI285380 q164d11.x
34	12.4	51.7	48	2	HS0003904
35	12.4	51.7	49	10	AI084829 ow89c12.s
36	12.4	51.7	52	10	AI284802 qu11h12.x
37	12.4	51.7	52	10	AI461385 fp44g03.x
38	12.4	51.7	52	10	AZ852502 2M0155D23
39	12.4	51.7	55	10	AA811401 0B82e07.s
40	12.4	51.7	57	10	AV543344 AV543344
41	12.4	51.7	57	13	B03160 CSR1-169H6-
42	12.4	51.7	58	10	AW247684 2820293.5
43	12.4	51.7	60	10	AI024966 cv39b10.x
44	12.4	50.8	21	13	AZ463806 1M0272G19
45	12.2	50.8	23	13	AZ336220 1M0066G19

ALIGNMENTS

RESULT 1
AI619480
LOCUS
DEFINITION
AI619480 40 bp mRNA EST
ty38g04.x1 NCI CGAP uc2 Homo sapiens cDNA clone IMAGE:2281398 3'
similar to WP:W03D2.1 CE14506 ; contains element MER22 repetitive
element ; mRNA sequence.

ACCESSION
AI619480
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-rt@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bdrrp/image/image.html

Trace considered overall poor quality
Insert length: 2989 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA-No.

FEATURES
Location/Qualifiers

source 1.40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2281398"
/clone_lib="NCI-CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
BASE COUNT 12 a 20 c 8 g 0 t
ORIGIN

Query Match 60.8%; Score 14.6; DB 10; Length 40;
Best Local Similarity 81.0%; Pred. No. 6.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 caaatggaaaacagctgcgc 24
|||||
Db 1 CAAGGGAACACCGCCGCC 21

RESULT 2
LOCUS AU104403 50 bp mRNA EST 05-APR-2001
DEFINITION AU104403 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP11308, mRNA sequence.
ACCESSION AU104403
VERSION AU104403.1 GI:13553924
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
TITLE Fine structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
JOURNAL Unpublished (2001)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="HEP11308"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT 5 a 12 c 19 g 14 t
ORIGIN

Query Match 60.0%; Score 14.4; DB 10; Length 50;
Best Local Similarity 75.0%; Pred. No. 7.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 cgacaatggaaaacagctgcgc 24
|||||
Db 24 CGACAATGCCCAACACATCC 1

RESULT 3
AI357794

LOCUS AI357794 55 bp mRNA EST 06-JAN-1999
DEFINITION qu98e04.x1 NCI-CGAP Gas4 Homo sapiens cDNA clone IMAGE:1980126 3', similar to TR:Q16038 Q16038 PRB1M PROTEIN, contains TRAI.t2 TRAI repetitive element, mRNA sequence.
ACCESSION AI357794 GI:4109415
VERSION AI357794.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 55)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbrr/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Glibco
High quality sequence stop: 1.
FEATURES
source 1..55
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1980126"
/clone_lib="NCI-CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11349-011"
BASE COUNT 14 a 23 c 18 g 0 t
ORIGIN

Query Match 60.0%; Score 14.4; DB 10; Length 55;
Best Local Similarity 75.0%; Pred. No. 7.3e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 cgacaatggaaaacagctgcgc 24
|||||
Db 18 CGCCAAAGGGAACCGCCGCC 41

RESULT 4
LOCUS AZ662129 45 bp DNA GSS 14-DEC-2000
DEFINITION IM0541J06F Mouse 10kb plasmid U0GCC1M library Mus musculus genomic clone U0GCC1M0541J06 F, DNA sequence.
ACCESSION AZ662129
VERSION AZ662129.1 GI:11799275
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

REFERENCE
AUTHORS

1 (bases 1 to 49)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

REFERENCE	AUTHORS
1 (bases 1 to 29)	
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,	
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly	

TITLE M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0110 row: 1 column: 18
 Seq primer: CACACGAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES

1. 29
 Location/Qualifiers

ORIGIN
 8 a 7 c 6 g 8 t
 Query Match 56.7%; Score 13.6; DB 13; Length 29;
 Best Local Similarity 80.0%; Pred. No. 1.7e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
LOCUS A1746720 31 bp mRNA EST 22-JUN-1999
DEFINITION u106f05.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:2065281 5' similar to TR:013953 O13953 HYPOPHYSICAL 39.1 KD PROTEIN C23H4.12 IN CHROMOSOME 1.; mRNA sequence.
ACCESSION A1746720
VERSION A1746720.1 GI:5124984
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 31)
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Mus.

AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
JOURNAL The WashU-NCI Mouse EST Project 1999
COMMENT Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:994469

FEATURES

1. 31
 Location/Qualifiers

ORIGIN
 2 a 10 c 9 g 10 t
 Query Match 55.8%; Score 13.4; DB 10; Length 31;
 Best Local Similarity 73.9%; Pred. No. 2e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 8
LOCUS A1026096 46 bp mRNA EST 27-AUG-1998
DEFINITION ov94h09.s1 Soares, J., NHT Homo sapiens cDNA clone IMAGE:1645025 3' similar to TR:Q62006 Q62006 OPA REPEAT; contains element L1 repetitive element.; mRNA sequence.
ACCESSION A1026096
VERSION A1026096.1 GI:3241709
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 46)
 Mammalia: Eutheria: Primates: Catarrhini: Homiinae: Homo.
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo
Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrrp/image/image.html

Trace considered overall poor quality
Insert length: 1791 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1. .46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1645025"
/clone_id="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - 01190(dT) primer (5'
TGTTACCAATCTGAATGGAGCGCCGCCAATTTTCTTTT 3').
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bernaldo."

BASE COUNT
ORIGIN

7 a 6 c 18 g 15 t

Query Match

55.88; Score 13.4; DB 10; Length 46;

Best Local Similarity 73.98; Pred. No. 1.9e+05;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

1 cgacaatggaataaacagctgc 23

Db 46 CGCAACTTCAACACACTCTC 24

RESULT 9

A2576214
LOCUS

A2576214 53 bp DNA

DEFINITION ASF-rp13SD-142 Genetrap T47D Human Breast Carcinoma Library Homo

ACCESSION

A2576214

VERSION

A2576214.1 GI:11562525

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

JOURNAL

Contact: Greg Henkel

COMMENT

Exon-trap tags from a T47D Genomescreen(TM) Library

COMMENT

Gene Expression

COMMENT

Aurora Biosciences Corp.

COMMENT

11010 Torreyana Road, San Diego, CA 92121, USA

COMMENT

Tel: 8584046436

COMMENT

Fax: 8584046719

COMMENT

Email: henkelg@aurorabio.com

COMMENT

Pools of cells were isolated from a Genomescreen(TM) library. The

library of cells was generated by retroviral integration of a gene

tagging element consisting of: 1) A promoterless beta-lactamase

proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3' RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAMP-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.

FEATURES

source

Location/Qualifiers

FEATURES

1. .53

FEATURES

/db_xref="taxon:9606"

FEATURES

/clone_lib="Genetrap T47D Human Breast Carcinoma Library"

FEATURES

/issue_type="Carcinoma"

FEATURES

/cell_type="Epithelial"

FEATURES

/note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA

FEATURES

from genetrapp pools: shotgun clone in pAMP-1 and used to

FEATURES

transform DH5-alpha competent bacteria."

FEATURES

29 a 13 c 3 g 8 t

FEATURES

Query Match

FEATURES

Best Local Similarity 73.98; Pred. No. 1.8e+05;

FEATURES

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

FEATURES

QY

FEATURES

1 cgacaatggaataaacagctgc 23

FEATURES

Db 16 CGCAAAATGGAACAACTTCAC 38

FEATURES

RESULT 10

FEATURES

R60882 55 bp mRNA EST 24-MAY-1995

FEATURES

LOCUS

FEATURES

DEFINITION

FEATURES

YH08F11.1 Soares infant brain INIB Homo sapiens cDNA clone

FEATURES

IMAGE:42503 5' similar to SP:C40793 C40793 PHOSPHORYLASE KINASE ;

FEATURES

mRNA sequence.

FEATURES

ACCESSION

FEATURES

R60882

FEATURES

VERSION

FEATURES

R60882.1 GI:831577

FEATURES

KEYWORDS

FEATURES

EST.

FEATURES

SOURCE

FEATURES

human.

FEATURES

Homo sapiens

FEATURES

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

FEATURES

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

FEATURES

1 (bases 1 to 55)

FEATURES

AUTHORS

FEATURES

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

FEATURES

, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

FEATURES

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston

FEATURES

, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Insert Size: 1831

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free

through LNL; contact the IMAGE Consortium (info@image.lnl.gov)

for further information. Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert length: 1831 Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 1.

Location/Qualifiers

1. .55

/organism="Homo sapiens"

/db_xref="GDB:415044"

/db_xref="taxon:9606"

/clone="IMAGE:42503"

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g11473211419b1Ar129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."									
BASE COUNT	1 a	5 c	3 g	18 t					
ORIGIN									
Query Match	55.0%;	Score 13.2;	DB 13;	Length 27;					
Best Local Similarity	83.3%;	Pred. No. 2.4e+05;							
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;					
Oy	1	cgaccaatggaanaacag 18							
Db	21	CGAAAAACGGAAGAG 4							
RESULT 12									
LOCUS	C21091	38 bp	mRNA	EST	23-OCT-1996				
DEFINITION	HMGSO002607 Human adult (K.Okubo) Homo sapiens CDNA 3', mRNA sequence.								
ACCESSION	C21091								
VERSION	C21091.1	GI:1622201							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 38)								
AUTHORS	Okubo,K.								
TITLE	BodyMap: human gene expression database								
JOURNAL	Unpublished (1995)								
COMMENT	Contact: Okubo,K. Institute for Molecular and Cellular Biol Osaka University 1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan Tel.: 06-877-5111(ex.3115) Email: kousakueimcb.osaka-u.ac.jp Human Gene Signature, 3'-directed CDNA sequence. We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones represented by this GS sequences is also found there.								
FEATURES	Location/Qualifiers								
source	1..38								
	/organism="Homo sapiens"								
	/db_xref="taxon:9606"								
	/clone_lib="Human adult (K.Okubo)"								
	/dev_stage="adult"								
BASE COUNT	16 a	6 c	6 g	10 t					
ORIGIN									
Query Match	55.0%;	Score 13.2;	DB 11;	Length 38;					
Best Local Similarity	83.3%;	Pred. No. 2.3e+05;							
Matches 15;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;					
Oy	5	aaatggaagaacgctcg 22							
Db	21	AAATGTAAAAACACCTGG 38							

RESULT 13
AA666844
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AA666844 59 bp mRNA EST 19-NOV-1997
vm65g11.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:1003172 5', mRNA sequence.
AA666844
AA666844.1 GI:2625545
EST
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 59)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:567388.

FEATURES
source
1.59
Location/Qualifiers
/organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:1003172"
/clone.lib="Knowles Solter mouse 2 cell"
/tissue.type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTGACCGTCGACCCCTTTTCTTTT-3'. CDNAS
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."

BASE COUNT
19 a 11 c 14 g 15 t

ORIGIN

Query Match 55.0%; Score 13.2; DB 10; Length 59;
Best Local Similarity 83.3%; Pred. No. 2, le+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 caaatggaataaacagctc 21
|||||
Db 2 CAAATGGAATTCACGCTC 19

RESULT 14
AT996547
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AT996547 60 bp mRNA EST 08-SEP-1999
701667389 A. thaliana, Columbia Col-0, root-1 Arabidopsis thaliana
cDNA clone 701667389, mRNA sequence.
AT996547
AT996547.1 GI:5843452
EST
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 60)
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
Wang,X., Hillman,J., Guebler,K., Kim,C., Doyle,M., Brzoska,P.,
Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R.,
Rose,M., Warren,B., Ton,B., Kasury,K., Borillo,C., Carpio,T.,
Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobrigh,A., Murry,L.,
Turner,C., Kirkorian,S., Elder,L. and Hanson,D.
Arabidopsis thaliana Gene Expression Microarray
Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.

FEATURES
source
1.60
Location/Qualifiers
/organism="Arabidopsis thaliana"
/cultivar="Columbia Col-0"
/db_xref="taxon:3702"
/clone="701667389"
/clone.lib="A. thaliana, Columbia Col-0, root-1"
/tissue.type="root"
/dev_stage="4 - 7 weeks"
/note="Vector: pSPORT. Site_1: NotI; Site_2: SalI; cDNA
library was derived from untreated root tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to SalI adaptors, digested with NotI,
size-selected, and cloned into the NotI and SalI sites of
the pSPORT vector."

BASE COUNT
23 a 12 c 1 g 20 t 4 others

ORIGIN

Query Match 55.0%; Score 13.2; DB 10; Length 60;
Best Local Similarity 78.9%; Pred. No. 2, le+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 cgacaaatggaataaacagc 19
|||||
Db 21 CNAACAATCCAAACATC 39

RESULT 15
AA476000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AA476000 34 bp mRNA EST 18-JUN-1997
vh26a02.r1 Soares mammary-gland NDMMG Mus musculus cDNA clone
IMAGE:876554 5' similar to SW:SCAA MOUSE P01863 IG GAMMA-2A CHAIN C
REGION. A ALLELE. ;, mRNA sequence.
AA476000
AA476000.1 GI:2203851
EST
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:516034

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. .34

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:876554"

/clone_1lb="Soares_mammary_gland_NDMG"

/sex="male"

/tissue_type="mammary gland"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'

TCTTACCAATCTGAAGTGGAGCGCGCGGATGGTTTTTTTTTTTTTTTTTT

T 3'); double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT773 vector.

RNA provided by Dr. Minoru Ko, Wayne State Univ. Library

constructed and normalized by Bento Soares and M.Fatima

Bonaldo."

BASE COUNT

7 a 12 c 5 g 10 t

ORIGIN

Query Match

54.2%; Score 13; DB 10; Length 34;

Best Local Similarity 76.2%; Pred. No. 2.8e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 gacaaatggaacagctcg 22

||||| ||||| ||||| ||

DB 28 GACAACTGATAGACAGATCG 8

Search completed: March 9, 2002, 00:09:10
Job time: 11026 sec